

L4 ANSWER 1 OF 1 MEDLINE  
 AN 96081515 MEDLINE  
 DN 96081515 PubMed ID: 8538493  
 TI A metallo-dependent **cysteine proteinase** of  
**Cryptosporidium** parvum associated with the surface of sporozoites.  
 AU Nesterenko M V; Tilley M; Upton S J  
 CS Division of Biology, Kansas State University, Manhattan 66506, USA.  
 NC AI30881 (NIAID)  
 SO MICROBIOS, (1995) 83 (335) 77-88.  
 Journal code: 0207257. ISSN: 0026-2633.  
 CY ENGLAND: United Kingdom  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 199602  
 ED Entered STN: 19960221  
 Last Updated on STN: 20000303  
 Entered Medline: 19960205  
 AB A proteinase of 24 kD was found associated with sporozoites of  
**Cryptosporidium** parvum. Optimal hydrolysis of azocasein, casein,  
 bovine serum albumin, and gelatin occurred at a pH of 6.5-7.0. Activity  
 against azocasein was inhibited by ethylenediaminetetraacetic acid (EDTA),  
 iodoacetic acid (IAA), trans-epoxysuccinyl-L-leucylamido(4-guanido) butane  
 (E-64), and phosphoramidon, suggesting that the enzyme was a  
 metallo-dependent **cysteine proteinase**. Both serine and  
 aspartate protease inhibitors failed to inhibit enzyme activity. The  
 enzyme was partially purified by preparative isoelectric focusing of  
 parasite membrane proteins. Polyclonal antiserum to parasite membrane  
 proteins was generated in rats. The enzyme-containing fraction was  
 subjected to SDS-PAGE and probed with antiserum, and the  
**antibodies** against the protease were eluted directly from  
 nitrocellulose blots. An indirect immunofluorescence assay using these  
 monospecific **antibodies** revealed that the protease occurred on  
 the surface of sporozoites, but was not associated with oocyst walls,  
 rhoptries, or micronemes.

(FILE 'HOME' ENTERED AT 15:55:09 ON 17 OCT 2002)

FILE 'MEDLINE' ENTERED AT 15:56:28 ON 17 OCT 2002

L1 618863 S ANTIBOD?  
L2 3245 S CRYPTOSPORIDIUM  
L3 14382 S CYSTEINE PROTEINASE# OR CATHEPSIN#  
L4 1 S L1 AND L2 AND L3

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L3 ANSWER 1 OF 1 MEDLINE  
 AN 95359407 MEDLINE  
 DN 95359407 PubMed ID: 7632919  
 TI Ethylene-regulated expression of a **carnation cysteine proteinase during** flower petal senescence.  
 AU Jones M L; Larsen P B; Woodson W R  
 CS Department of Horticulture, Purdue University, West Lafayette, IN 47907-1165, USA.  
 SO PLANT MOLECULAR BIOLOGY, (1995 Jun) 28 (3) 505-12.  
 Journal code: 9106343. ISSN: 0167-4412.  
 CY Netherlands  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 OS GENBANK-U17135  
 EM 199509  
 ED Entered STN: 19950921  
 Last Updated on STN: 20000303  
 Entered Medline: 19950912  
 AB The senescence of carnation (*Dianthus caryophyllus* L.) flower petals is regulated by the phytohormone ethylene and is associated with considerable catabolic activity including the loss of protein. In this paper we present the molecular cloning of a cysteine proteinase and show that its expression is regulated by ethylene and associated with petal senescence. A 1600 bp cDNA was amplified by polymerase chain reaction using a 5'-specific primer and 3'-nonspecific primer designed to amplify a 1-aminocyclopropane-1-carboxylate synthase cDNA from reverse-transcribed stylar RNA. The nucleotide sequence of the cloned product (pDCCP1) was found to share significant homology to several cysteine proteinases rather than ACC synthase. A single open reading frame of 428 amino acids was shown to share significant homology with other plant cysteine proteinases including greater than 70% identity with a cysteine proteinase from *Arabidopsis thaliana*. Amino acids in the active site of cysteine proteinases were conserved in the pDCCP1 peptide. RNA gel blot analysis revealed that the expression of pDCCP1 increased substantially with the onset of ethylene production and senescence of petals. Increased pDCCP1 expression was also associated with ethylene production in other senescing floral organs including ovaries and styles. The pDCCP1 transcript accumulated in petals treated with exogenous ethylene within 3 h and treatment of flowers with 2,5-norbornadiene, an inhibitor of ethylene action, prevented the increase in pDCCP1 expression in petals. The temporal and spatial patterns of pDCCP1 expression suggests a role for cysteine proteinase in the loss of protein during floral senescence.

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1291 DROUGHT  
35815 INDUCIBLE

L2 1 ENCODE DISTINCT DROUGHT INDUCIBLE  
(ENCODE (W) DISTINCT (W) DROUGHT (W) INDUCIBLE)

=> D BIB AB

L2 ANSWER 1 OF 1 MEDLINE

AN 93314960 MEDLINE

DN 93314960 PubMed ID: 8325504

TI Structure and expression of two genes that **encode distinct drought-inducible** cysteine proteinases in *Arabidopsis thaliana*.

AU Koizumi M; Yamaguchi-Shinozaki K; Tsuji H; Shinozaki K

CS Laboratory of Plant Molecular Biology, Tsukuba Life Science Center, Institute of Physical and Chemical Research (RIKEN), Ibaraki, Japan.

SO GENE, (1993 Jul 30) 129 (2) 175-82.

Journal code: 7706761. ISSN: 0378-1119.

CY Netherlands

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals; Space Life Sciences

OS GENBANK-D13042; GENBANK-D13043; GENBANK-L03653; GENBANK-L03654;

GENBANK-L05530; GENBANK-L07632; GENBANK-M96931; GENBANK-M96932;

GENBANK-M96933; GENBANK-X54209

EM 199308

ED Entered STN: 19930820

Last Updated on STN: 20010625

Entered Medline: 19930812

AB Among nine cDNA clones (named RD) corresponding to genes that are responsive to dehydration in *Arabidopsis thaliana*, two clones, RD19 and RD21, were analyzed further. Northern blot analysis revealed that both the RD19 and RD21 mRNAs were not induced by abscisic acid. Neither RD19 nor RD21 mRNA synthesis was responsive to cold or to heat stress. On the other hand, transcription of both the RD19 and RD21 mRNAs was strongly induced under high-salt conditions, which suggests that the genes corresponding to RD19 and RD21 may be induced by changes in the osmotic potential of plant cells. Putative proteins, RD19 and RD21, encoded by two of the RD cDNAs have amino acid (aa) sequences typical of the catalytic sites of cysteine proteinases (CysP). RD21 and RD19 appeared to contain signal peptides that function in protein secretion. RD21 contains an aa sequence similar to that of the C-terminal extension peptide. Phylogenetic tree analysis indicated that the putative RD21 and RD19 proteins are quite different types of CysP. Genomic Southern analysis revealed that each gene family contains at least two members, which do not cross-hybridize. The two genes corresponding to RD19 and RD21 (rd19A and rd21A, respectively) were cloned and their structural analysis revealed the presence of two and four introns, respectively. The numbers and sites of introns differ between the genes, supporting our hypothesis that rd19A and rd21A belong to different subfamilies of genes encoding CysP. The transcription start points were determined by primer extension. Two conserved sequences were found in the promoter regions of the two genes.

L6 ANSWER 1 OF 1 MEDLINE  
 AN 97094976 MEDLINE  
 DN 97094976 PubMed ID: 8939744  
 TI The **prosequence** of **procaricain** forms an alpha-helical domain that prevents access to the substrate-binding cleft.  
 AU Groves M R; Taylor M A; Scott M; Cummings N J; Pickersgill R W; Jenkins J A  
 CS Department of Food Macromolecular Science, Institute of Food Research, Reading, UK.  
 SO STRUCTURE, (1996 Oct 15) 4 (10) 1193-203.  
 Journal code: 9418985. ISSN: 0969-2126.  
 CY ENGLAND: United Kingdom  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 OS PDB-1PCI; PDB-R1PCISF  
 EM 199701  
 ED Entered STN: 19970219  
 Last Updated on STN: 20000303  
 Entered Medline: 19970128  
 AB BACKGROUND: Cysteine proteases are involved in a variety of cellular processes including cartilage degradation in arthritis, the progression of Alzheimer's disease and cancer invasion: these enzymes are therefore of immense biological importance. Caricain is the most basic of the cysteine proteases found in the latex of *Carica papaya*. It is a member of the papain superfamily and is homologous to other plant and animal cysteine proteases. Caricain is naturally expressed as an inactive zymogen called procaricain. The inactive form of the protease contains an inhibitory proregion which consists of an additional 106 N-terminal amino acids; the proregion is removed upon activation. RESULTS: The crystal structure of procaricain has been refined to 3.2 Å resolution; the final model consists of three non-crystallographically related molecules. The proregion of caricain forms a separate globular domain which binds to the C-terminal domain of mature caricain. The proregion also contains an extended polypeptide chain which runs through the substrate-binding cleft, in the opposite direction to that of the substrate, and connects to the N terminus of the mature region. The mature region does not undergo any conformational change on activation. CONCLUSIONS: We conclude that the rate-limiting step in the *in vitro* activation of procaricain is the dissociation of the prodomain, which is then followed by proteolytic cleavage of the extended polypeptide chain of the proregion. The prodomain provides a stable scaffold which may facilitate the folding of the C-terminal lobe of procaricain.

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L8 ANSWER 1 OF 1 MEDLINE  
 AN 97051808 MEDLINE  
 DN 97051808 PubMed ID: 8896443  
 TI Structure of **human procathepsin L**  
**reveals** the molecular basis of inhibition by the prosegment.  
 AU Coulombe R; Grochulski P; Sivaraman J; Menard R; Mort J S; Cygler M  
 CS Biotechnology Research Institute, National Research Council of Canada,  
 Montreal, Quebec.  
 SO EMBO JOURNAL, (1996 Oct 15) 15 (20) 5492-503.  
 Journal code: 8208664. ISSN: 0261-4189.  
 CY ENGLAND: United Kingdom  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 199612  
 ED Entered STN: 19970128  
 Last Updated on STN: 20020420  
 Entered Medline: 19961206  
 AB Cathepsin L is a member of the papain superfamily of cysteine proteases  
 and, like many other proteases, it is synthesized as an inactive  
 proenzyme. Its prosegment shows little homology to that of procathepsin B,  
 whose structure, the first for a cysteine protease proenzyme, has been  
 determined recently. We report here the 3-D structure of a mutant of human  
 procathepsin L determined at 2.2 A resolution, describe the mode of  
 binding employed by the prosegment and discuss the molecular basis for  
 other possible roles of the prosegment. The N-terminal part of the  
 prosegment is globular and contains three alpha-helices with a small  
 hydrophobic core built around aromatic side chains. This domain packs  
 against a loop on the enzyme's surface, with the aromatic side chain from  
 the prosegment being located in the center of this loop and providing a  
 large contact area. The C-terminal portion of the prosegment assumes an  
 extended conformation and follows along the substrate binding cleft toward  
 the N-terminus of the mature enzyme. The direction of the prosegment in  
 the substrate binding cleft is opposite to that of substrates. The  
 previously described role of the prosegment in the interactions with  
 membranes is supported by the structure of its N-terminal domain. The fold  
 of the prosegment and the mechanism by which it inhibits the enzymatic  
 activity of procathepsin L is similar to that observed in procathepsin B  
 despite differences in length and sequence, suggesting that this mode of  
 inhibition is common to all enzymes from the papain superfamily.

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